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ZEHNDER Marc

Molecular phylogenetic analysis of the tapeworm order Proteocephalidea based on mitochondrial 16S rDNA sequences

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(alphabetically by first author)

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Natal dispersal in a metapopulation of house sparrows (*Passer domesticus*); characteristics and fate of the dispersing individuals

In this study, we examine dispersal between local populations in a metapopulation of house sparrows (*Passer domesticus*) on an archipelago in Northern Norway. The following questions were addressed: 1) Is dispersal random movement, or is it influenced by the spatial arrangement of the islands? Are there differences in dispersal tendency or dispersal distance between age classes and between the sexes? 2) What is the relationship between dispersal probability and variation in several traits that are important for life history in birds, and 3) How do dispersers perform compared to residents in terms of survival. The observed distribution of dispersal distances differed significantly from the expected distribution under the assumption of equal colonization and emigration rates across islands. Dispersal was more intense among less isolated islands. In accordance with the general trend in passerine birds, dispersal was almost exclusively performed by juveniles. There was no significant sex bias in dispersal tendency and dispersal distance. Among females, dispersers tended to be larger and had higher adult survival compared to residents. Among males, early hatched and low ranking individuals were more likely to disperse. They did not differ from resident males in adult survival rate but had lower survival than female dispersers. Dispersal seemed thus to be performed by viable and successful females, and by subordinate males. These results indicate that dispersal within the studied metapopulation is a phenomenon influenced by many factors which may act in different ways on different parts of the population.

AVISE John

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The history and purview of phylogeography

About 10 years have passed since the birth of phylogeography as a formal discipline. However, the field's gestation began in the mid-1970's with the introduction of mitochondrial DNA analyses to population genetics, and to the profound shift toward genealogical thought at the intraspecific level (now formalized as coalescent theory) that these methods prompted. Here, I will briefly trace the history and explosive growth of phylogeography, consider some of the conceptual ramifications of the field for conservation and population biology, and close with a few thoughts on future challenges for the discipline.

BAIROCH Amos

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How can protein sequence database be helpful for phylogenetic studies

No abstract available.

BALLABENI Pierluigi, CONCONI Davide & RAHIER Martine

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Oviposition preference and larval performance in a leaf beetle
No abstract available.

BALLOUX François, GOUDET Jérôme & PERRIN Nicolas

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Breeding system and genetic variance in the monogamous, semi-social shrew, *Crocidura russula* (Insectivora, Soricidae)

The population-genetics consequences of monogamy and male philopatry (a rare breeding system in mammals) were investigated in the semi-social and anthropophilic shrew *C. russula* with the use of microsatellite markers. Genetic diversity was large ($H=0.813$) with significant differentiation among subpopulations (5-6%) over a small geographical scale (16 km). Subpopulations were themselves structured into smaller units («breeding groups») comprising an estimate of four breeding pairs each. Members of the same breeding groups displayed significant coancestries (9-10%), essentially due to strong male kinship: syntopic males were on average related at the half-sib level. Female dispersal among breeding groups was not complete (estimate 39%), and insufficient to prevent inbreeding. From our results, the breeding strategy of *C. russula* seems less efficient than classical mammalian systems (polygyny and male dispersal) in disentangling coancestry from inbreeding, but much more so in boosting the effective size of subpopulations, and thereby retaining genetic variance.

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Phenotype and individual investment of cooperating ant queens

Fire ant (*Solenopsis invicta*) queens founding a colony with unrelated nestmates potentially face a trade-off. Increased individual investment enhances worker production, colony survival and growth. However, increased investment may reduce a queen's probability of surviving fights that invariably arise after worker eclosion. Indeed, previous studies showed that (i) queens lose less weight (a measure of investment) when initiating colonies with cofoundresses than when alone and (ii) within associations the queen losing more weight is more likely to die. In this study, we tested whether queens adjust weight loss to social environment and fighting ability, and whether restraining weight loss directly increases survival prospects. Experimental manipulation of colonies showed that reduced investment by queens within associations is primarily a response to the presence of a nestmate and not simply a response to differences in per-queen brood care demands. Differences in head width were associated with relative and combined weight loss of cofoundresses, as well as queen survival. Manipulation of the queens' relative weight by feeding and exposure to contrasting social environment (queens kept alone or in groups) did not significantly affect survival. These results indicate that head width differences, or other correlated phenotypic attributes of fighting ability, influenced both investment strategies and survival probability of queens. That the queens with larger heads both invested less energy into brood rearing and were more likely to survive suggests that early foundress associations of ants may not be as peaceful as previously assumed.

BERNASCONI Marco^{1,2}, VALSANGIACOMO Claudio², PIFFARETTI Jean-Claude² & WARD Paul¹

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autumn. This about 5 km² big area called «Widen» is intensively used agricultural land, characterized by a relatively high abundance of «ökologische Ausgleichsflächen» and small mammal numbers. I could show that the winter distribution and movements of the Kestrels were not only due to the weather situation but also to the combined influence of habitat distribution and quality, perch availability as well as vole abundance and distribution.

To support our overwintering Kestrels it seems to be essential to lay out further «ökologische Ausgleichsflächen» and bigger extensively cultivated areas in combination with erecting more perches.

CASTELLA Vincent, GOUDET Jérôme & PERRIN Nicolas

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Allozyme variance and habitat in the freshwater snail *Physa acuta*

The wide-spread freshwater Gastropod *Physa acuta* colonizes big lakes as well as small, temporary ponds. Both habitats show a pronounced difference in temporal and spatial structure. Populations living in these two distinct habitats might then be genetically differentiated.

460 snails were collected from 12 different sites, six sites being of lake habitats (Léman and Neuchâtel) and six sites being of pond habitats. All individuals were genotyped using six polymorphic allozyme loci.

Differentiation was high between ponds' populations. Despite their low dispersal abilities snails from the lake Léman were genetically weakly differentiated. All populations showed a strong heterozygotes deficiency which was independent of their environment. This suggests that this deficiency is due to selfing and consanguineous matings. In spite of their recent colonization, the genetic variability of some pond's populations was as high as those from the lakes. The presence of two genetically different gene pools between these distinct habitats suggests the existence of two sibling species or the possible action of selection.

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Molecular Phylogeny and Biogeography of the Genus *Ilex* L. (Aquifoliaceae)

The genus *Ilex* L. (Aquifoliaceae) contains about 600 species of trees and shrubs distributed worldwide with a maximum diversification in east Asia and south America. It is a quite ancient genus, with fossils known from 90 my ago. The phylogeny of *Ilex* has been investigated using chloroplastic DNA. The atpB/rbcL spacer has been sequenced for 110 species. For 41 of these species, the rbcL gene has been sequenced in addition to the spacer. The phylogenies inferred from this database are presented, and their implications for the taxonomy and biogeography of the genus are discussed. In general, this genus appears to be a difficult taxon to study. In particular, the taxonomical treatments published by classical authors show only limited correlation with the molecular information. The biogeographical interpretation of the molecular phylogenies is problematic too. These difficulties may arise from the very long history of the genus, in which many extinctions and subsequent radiations have probably blurred the patterns that could have existed.

CURCIC Bozidar P. M. & MAKAROV Slobodan

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Endemic differentiation of millipedes (Diplopoda, Myriapoda) in Serbia, Montenegro and Macedonia: taxonomic implications

The fauna of diplopods in Serbia, Montenegro and Macedonia is very rich and diverse. Out of 136 species inhabiting the areas studied, 48 (or 35.29%) are endemic to these regions; furthermore, of 48 genera, only 4 (or 8.33%) are endemic to the same areas, but none of the families. In Serbia, 70 diplopod species have been found, and 59 and 59 in Montenegro and Macedonia, respectively. There exist no endemic genera in Serbia, but Montenegro and Macedonia are inhabited by 1 and 3 endemic general respectively.

Serbia, Macedonia and Montenegro have in common 33 species, 23 genera and 14 families of diplopods. Serbia and Montenegro are inhabited by 18 common species, 15 genera and 9 families, while Serbia and Macedonia have in common 29 species, 21 genus and 13 families; and Montenegro and Macedonia are characterized by shared 16 species, 12 genera and 7 families. There are neither endemic species nor genera shared either by Serbia and Montenegro or by Montenegro and Macedonia. Only 5 endemic species and 1 genus are endemic both to Serbia and Macedonia; these are: *Albanoglossus ljubetensis* Attems, *Brachydesmus (Stylobrachydesmus) ljubetensis* Attems, *Xestoiulus (Oroiulus) macedonicus* (Attems), *Megaphyllium crassum* (Attems) and *Typhloiulus (Typhloiulus) albanicus* Attems. The majority of endemic diplopods in the areas studies belong to the families Polydesmidae (16 species, or 33.33% of all endemic forms), and Julidae (14 species, or 29.17% of all endemic forms).

The abundance of both higher and lower taxa of endemic diplopods in Serbia, Montenegro and Macedonia may be partly explained by the long-lasting tectonic movements by the folding and faulting processes, by the epeirogenetic movements and by the evolution of the karstic relief which have greatly influenced the distribution of the ancient diplopod fauna in the Balkan Peninsula.

In conclusion, Serbia, Montenegro and Macedonia are inhabited by an extremely varied fauna of endemic diplopods pertaining to different phyletic lineages; these forms are of different origins and ages. Therefore the Balkan Peninsula represents one of the main global centres of endemic differentiation of the millipede fauna.

CURCIC Bozidar P. M. & MAKAROV Slobodan

Institute of Zoology; Faculty of Biology; University of Belgrade; Studentski Trg 16; 11000 Belgrade; Yugoslavia

On geographic distribution and historical development of some cave-dwelling diplopods (Myriapoda) in Serbia, Montenegro and Macedonia (FYROM)

The analysis of geographic distribution and taxonomic interrelationships of cave millipedes has clearly shown that Serbia, Montenegro and Macedonia are characterized by an extremely rich and diverse diplopod fauna inhabiting the underground habitats of the areas studied. Therefore, this study has shown that each of these regions is inhabited by 16, 8, and 3 cavernicolous species, classified into 9, 5, and 2 genera, and 7, 5, and 2 families, respectively. Each endemic species is restricted to one of the areas studied. A single genus is common both to Serbia and Montenegro, while no genera have been found either common to Serbia and Macedonia, or to Montenegro and Macedonia, respectively. Only one millipede family is common both to Serbia and Macedonia, as well as to Montenegro and Macedonia, respectively; additionally, two diplopod families are common both to Serbia and Montenegro. Of all cave species, 13 troglobitic forms inhabit Serbia (3 are either troglaphiles or troglloxenes), 6 - Montenegro (2 are troglaphiles and troglloxenes), and 1 - Macedonia (2 troglloxene and troglaphile species).

The underground diplopods of Serbia, Montenegro, and Macedonia are probably the remains of some ancient hygrophilic forms. With the climatic changes (and the subsequent increase of aridity) and the origin and development of different niches, these forms evolved as cave inhabitants. However, the main reasons for the outstanding variety of cave diplopods in the Balkan Peninsula (including the areas studied) are: the presence of a varied diplopod fauna once inhabiting the Proto-Balkans, the evolution of the underground karstic relief, the favourable climatic changes and the subsequent radiation of the diplopod taxa in numerous isolated habitats.

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Cryptic diversity in the open Ocean

To estimate the biodiversity of the open ocean and to understand how speciation can occur in such a homogeneous environment mixed by water currents, is a new deal for oceanography. We have examined the genetic diversity in the foraminifer *Orbulina universa*, one of the most commonly encountered planktonic organism inhabiting the world Ocean between 50° N and 50° S. This species appeared in the fossil record 16 Myr ago and is largely used as a stratigraphic and paleoclimatic index. By sequencing SSUrRNA genes of several specimens collected in 33 stations across the Atlantic, we have shown large and geographically localized genetic differences among *O. universa*. This variability reveals three cryptic allopatric species, adapted to different water masses. The molecular timing of their speciation is compared to the history of the Atlantic.

DEVORE-SCRIBANTE Ariane

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The Pseudoscorpions (Arachnida) of Switzerland: systematic, faunistic and biogeographical study

Presently, 58 species of pseudoscorpions are recorded from Switzerland, 13 of which are recorded for the first time from this country.

The aims of the present study are:

- to provide a detailed description of male, female and the 3 postembryonic stages, of each species,
- to examine the taxonomic status of each species and to give reliable keys for the Swiss fauna,
- to complete to knowledge the distribution (maps) and the ecology of the treated species.

The systematic study includes morphometrical measures and chaetotaxy (tables); the diagnostic characters are figured.

The distributional data are based on the material of the collection of the Museum of Natural History, Geneva.

Switzerland, due to its specific position in Europe enhances the presence of a large range of species with different distributions patterns:

- the widely distributed and cosmopolitan-type
- the Mediterranean-type (South of Alps)
- the eastern-type (North-East)
- the western-type (along the Jura mountain)
- the alpine-type
- the endemics and apparent endemics (cavernicolous and other species from specific localities).

DIETRICH Barbara & WEHNER R.

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Parapatric distribution of desert ants: Inter- and intraspecific variation of mitochondrial DNA of desert ants, *Cataglyphis* Foerster, 1950

The ants of the genus *Cataglyphis* are a highly specialized species, which inhabit the food impoverished areas of the Old World deserts. *Cataglyphis* has evolved amazing navigational abilities to cope with this scanty environment. The three prominent species of the *bicolor* group, formerly described as one species ("bicolor"), show a strongly parapatric North-South distribution (Wehner, R. *et al.* 1994: Senckenbergia biologica 74: 163).

Restriction fragment length polymorphism (RFLP) analysis of mitochondrial DNA (mt-DNA) was chosen as the technique to investigate the ants population structures on a molecular basis. In within species comparisons mt-DNA phylogenies have been proven useful in population studies as well as in the defining themselves. Many disadvantages of traditional RFLP analysis for analysing population variation using individual insects, such as the small amount of DNA, are eliminated by carrying out polymerase chain reactions (PCR) in advance. Two primer pairs were used (CoI->CoII, N1NFA->CB3FC) to amplify the mt-DNA sequences. To cut them we used three restriction enzymes DraI, SspI and TaqI.

Ants of eleven different *C. bicolor* populations (oasis- and steppe populations) were analysed. A comparison between populations from continuous and disruptive habitats showed that these two population series hardly differ.

The results of genetic variation in different populations of *C. bicolor* were compared with the results received by examining closely related species of the same genus (*C. savignyi*, *C. viaticus*, *C. velox* and *C. rosenhauri*). Especially the N1NFA->CB3FC sequence confirms that all species of the bicolor group are clearly distinct species. Methodically the results reveal which part of the mt-DNA of *Cataglyphis* is effective in resolving the phylogeny and population structures of the bicolor species group.

DONOGHUE Michael J.

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Phylogenies, TreeBASE, and comparative biology

Many evolutionary studies require access to multiple phylogenetic trees. I will illustrate a variety of such studies, including analyses of (1) general patterns in homoplasy, (2) change in particular characters over composite phylogenies (supertrees), (3) the sensitivity of particular comparative results to alternative phylogenetic hypotheses, (4) gene trees with respect to species trees, and (5) species trees with respect to biogeography and conservation. Access to original phylogenetic data is needed for reanalysis with the same or with different methods, and for the combination of different sources of evidence. In view of such needs, the development of databases of phylogenetic knowledge should be a high priority, yet this endeavor has received little attention. I will briefly describe the TreeBASE database in order to explore a number of issues surrounding the design and use of a database of published trees and data matrices.

DONZE Gérard

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Do non-hosts help Swallowtail butterflies to find their host plants?

Most caterpillars will only grow on a limited range of plant species so that the biochemical tolerance of larvae and female oviposition must be in accordance even as they are distinct physiological processes. Host choice by females is crucial for the survival of first instar caterpillars which are themselves unable to select a host. When searching for host plants, in a pre-landing phase, females receive visual and olfactory inputs. After landing on a plant, the female can further assess the quality of the plant by mechanical and gustatory stimuli. The efficiency of the host-finding depends on the ability to quickly differentiate the non-host species from suitable host plants.

I have studied the pre-landing perception of plants by butterflies and hypothesized that *Papilio polyxenes* (Papilionidae) females use their previous experiences (i.e., both acceptances and

rejections) in order to enhance their judgement. We tested this hypothesis using olfactory cues from a host plant, the carrot (*Daucus carota*), and from a non-host plant, the yarrow (*Achillea millefolium*). To simplify the model, I controlled visual stimuli (i.e., shape and color) and gustatory stimulants with the help of model plants cut from sponge. The results showed that experienced females, which had previously had been in contact with both the host and the non-host plants, were better able to avoid landings on sponges odorified with no-host odour compared to females which had contact only with the host plant.

As the sensory input is multi-modal, and since insects are able to learn, use of previous positive and negative experiences reduces the error of landings on plants unsuitable for their caterpillars.

DUBOULE Denis

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Regulation and function of vertebrate Hox genes during limb development and evolution

The function of *Hoxd* genes during development and their potential role in the evolution of the vertebrate limb has been studied in two different systems. In mice, single, double as well as triple inactivations (cre-mediated deletions) have been produced to assess the function of these genes during development. The results demonstrate that *Hoxd* genes act in a coordinated and cooperative way, where quantitative interactions seem to be at least as important as qualitative ones. In a different approach, we analysed the development of fish appendicular skeletons. Pectoral fins are the appendicular structures which are, in fishes, homologous to the tetrapod forelimbs. We initiated a comparative study in lower vertebrates in the aim of understanding the ontogenetic and phylogenetic relationships between these two structures. We have undertaken a detailed analysis of the development of the endoskeletal component of the pectoral fins of the zebrafish (*Danio rerio*). The sequence of appearance of the various mesenchymal prechondrogenic condensations has been determined as well as the mitotic dynamics in the mesenchymal sheets. In parallel, we cloned and characterized the posterior halves of the fish *HOXA* and *HOXD* complex, i.e. the *Hoxd-9* to *d-13* genes as well as the *Hoxa-9* to *Hoxa-13* genes. These genes were shown, in mammals, to play an important function in limb pattern formation. The expression of these genes during pectoral fin development were analysed in details and compared to the expression of a potential morphogen molecule encoded by the fish gene *hedgehog*. The significance of these results will be discussed in the light of the current theories (mainly derived from paleontological data) which account for the fin to limb transitions. The fin to limb transition will be taken as an example to illustrate some aspects of the functional organization of the *Hox* gene family in vertebrates, in relation with the evolution of functions. In particular, the involvement of this genetic system both in the evolution of morphologies through heterochrony and in the maintenance of a vertebrate body plan will be discussed.

DUPANLOUP Isabelle, SCHNEIDER Stefan & EXCOFFIER Laurent

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Inferring genetic impact of cultural and ecological barriers: a new approach

Several techniques have been developed to detect the presence of genetic boundaries which can be defined as areas where the rate of change of gene frequencies is particularly high. These boundaries may correspond to either steep ecological gradients or regions of limited gene flow between populations. Sometimes these frontiers are even defined a priori based on non genetic factors like ecology, geography or culture. We present here a new method to infer the biological impact of these frontiers on gene flow between populations.

Because the processes acting on different portions of the frontier may be heterogeneous, we first divide the frontier into segments of arbitrary sizes and then evaluate the "permeability" of each segment independently. For each segment, we compute a statistic equivalent to the proportion of genetic distances between samples located on different sides of the barrier that are larger than the distances between samples located on the same side of the barrier taking into account the observed geographic distances between samples. The confidence intervals of this statistic are also evaluated. The program output is a graphical representation of the populations and of the frontier: the width of the segments of the frontier is drawn proportional to the statistic computed for this segment and to its statistical significance.

FAUCCI Anuschka

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Structure of a hydroid-seaweed community

Epiphytism is a strategy for opportunistic species to escape high competition in marine hard bottom communities. In the present study the seasonal and spatial distribution of epiphytic hydroids on three species of the widespread brown algae *Cystoseira* have been investigated on two sites of different water exposure at the rocky shore of Porto Cesareo (Ionian Sea/Italy). The addressed questions were:

- 1) Is there seasonal pattern in the hydroid community on *Cystoseira*?
- 2) Which factors influence the community structure: a) exposure to wave action? b) substrate differences?
- 3) Do the more fragile athecate hydroids occur at different sites than thecate hydroids?

Ordination by Canonical Correspondence Analysis (CCA) was used to summarize the variation in species composition and frequency related to site and date. The two sites of different exposure are clearly separated and show a seasonal cycle. The algal stems from the exposed site are shorter and less colonized than the one from the sheltered site. Exposure to wave action has a bigger influence on the community than the differences in algal substrate. Athecate hydroids prefer clearly sites with less wave action and higher structured algae, i.e. sites with less mechanical stress than thecate hydroids.

FLOOK Paul K. & Rowell C. H. F.

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Examining hypotheses of grasshopper evolution with molecular sequence data

We have used nuclear and mitochondrial DNA sequences to examine the systematics of the insect order Orthoptera. Phylogenies reconstructed from the molecular data have proved robust at different taxonomic levels and have enabled us to make inferences about various aspects of orthopteran evolution. An important finding of the work concerns the phylogeny of the superfamily Acridoidea (true grasshoppers and relatives). Analysis of a large, representative taxonomic sample indicates that mtDNA sequences of several of the major acridoid lineages have diverged to an approximately equal degree. One interpretation of this pattern is that the major acridoid groups arose simultaneously during evolution. Alternatively, the observed similarity in branch lengths separating members of different lineages may reflect site saturation in the mtDNA sequences. We have examined the two possibilities by

- (i) comparing sequence divergence within acridoid lineages;
- (ii) comparing sequence divergence between other orthopteran groups;
- (iii) estimating rates of intra-specific variability;
- (iv) analysing patterns of among site rate variation, and;
- (v) analysing the assumption of substitution rate constancy.

We conclude that the observed pattern of sequence divergence does reflect a sudden radiation of acridoid species. The analyses also indicate that the mtDNA sequences are evolving at an

approximately equal rate, allowing us to make inferences concerning the ages of the main acridoid groups. We discuss the implications of these findings for our understanding of orthopteran evolution and relate the results to existing systematic hypotheses.

FREY Daniel

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RAPDs reveal extensive genetic variability in the apomictic *Erigeron annuus*

Erigeron annuus is considered an obligate apomictic taxa of the Asteraceae. It is native in eastern North America and has successfully spread all over the world, mainly the northern hemisphere. Four RAPD primers were used to assess genetic variability in about 800 individuals from a total of 100 Western European sampling locations. Up to 35 distinct and reliable bands were found per primer, most of them polymorphic. Different approaches were used to assess intra- and interpopulation variability, such as an analysis of molecular variance (AMOVA) and spatial autocorrelation analysis. Preliminary results are presented.

GALLAND Nicole, SAVOLAINEN Vincent, SALAMIN Nicolas & SANJOVO Alexandre

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Phylogeographic relationships among the polyploid complex *Ornithogalum umbellatum* (Liliaceae), based on allozyme and RAPD data

O. umbellatum forms a polyploid complex in Mediterranean and temperate Europe. Several former "species" have been recognized as 3 infraspecific entities: morph 1 (2x), morph 2 (3x) and morph 3 (4x, 5x, 6x). A close taxon, *O. algeriense* (6x) was identified as a separate species in Northern Africa and Southern Spain. The study of allozyme variation allows to confirm the conspecific nature of all diploids; their genetic distances are highly correlated with geographic distances, suggesting a trend to geographic speciation. Allozyme patterns of polyploids suggest an autopolyploid origin for *O. umbellatum*, whereas *O. algeriense* displays a fixed heterozygosity typical for an amphiploid origin. RAPDs were used to look for clusterings within the *Ornithogalum* complex: their use turned out to be informative for the segregation of *O. algeriense* and the remaining *umbellatum* s. str. A comparison of the informativity of RAPDs versus allozymes is presented in this context.

GANTENBEIN Benjamin & SCHOLL Adolf

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Allozymes show an unusually high genetic differentiation of *Euscorpius germanus* (Scorpiones: Chactidae) populations

We examined the genetic population structure of *Euscorpius germanus* (C. L. Koch, 1837) using horizontal starch gel enzyme electrophoresis (18 loci surveyed). We collected eight population samples from Switzerland (Valais, Ticino, Grison), 19 samples from northern Italy (Lombardia, Trentino, Alto Adige), and two samples from Austria (Carinthia). These samples include the subspecies *E. g. germanus* (C. L. Koch, 1837) and *E. g. alpha* di Caporiacco, 1950. Eight of the north Italian samples come from the Valle Brembana (Alpi Bergamasci), where Bonacina (1980) suggested hybridization between the two subspecies, based on asymmetric numbers of trichobothria on the pedipalp tibia and of the pectinal teeth. We included four samples of *E. flavicaudis* (de Geer, 1778), two samples of *Buthus occitanus* (Amoreux, 1789), and four samples of *Mesobuthus gibbosus* (Brullé, 1832) for comparison. The analysis revealed two highly differentiated population groups in *E. germanus* which are separated by the river

Etsh in northern Italy. These population groups are fixed for alternative alleles at eight out of 18 gene loci and coincide roughly with the subspecies *E. g. germanus* and *E. g. alpha*. However, there is no evidence of introgressive hybridization from the allozyme data. The easternmost population from Austria (Carinthia, Karawanken) indicates a third population group that is separated from the former groups by allele substitution at nine out of 18 gene loci. In the phenogram (UPGMA cluster analysis using Nei's (1972) genetic distance), the branching points of the *E. germanus* population groups are found at unusually high distances as compared to the outgroup taxa.

GOUDET Jérôme & SAVOLAINEN Vincent

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Key innovations and rate of speciation: statistical artefact or real phenomenon?

Investigations have often shown that key innovations such as phytophagy in insects or nectar spurs in angiosperms have led to an increased rate of speciation. Recently, evidence for correlation in the rate of microevolution (e.g. number of mutations along the branches in a cladogram) and macroevolution (number of species in families connected to these branches) was found. Here we review the statistical methods use to put forward these claims and suggest a new test. Extended data in angiosperms show that, despite tending toward a positive correlation between rate of micro and macroevolution, this relation is severely influenced by the taxonomies employed, the phylogenetic sampling and in turn the accuracy of the phylogenies.

GRIFFIN Andrea

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Updating the path integrator through a visual fix

To survive and to reproduce it is essential for any sedentary animal to know its way around its environment. Indeed it must be able to relocate reliable food sources, shelter and water, avoid predators, find mates and provision offspring. Mammals can navigate through path integration (dead reckoning) by updating their position on the basis of internal signals generated during locomotion, without using any external references. However, being open to cumulative errors, path integration remains functional over short excursions only, unless it is corrected by positional information from familiar landmarks. The hypothesis that reference to learned landmarks can update the path integrator was examined in golden hamsters (*Mesocricetus auratus* W.) during hoarding excursions occurring in darkness, within a large open arena. The subjects proceeded from their peripheral nest to a platform located at one of seven feedingsites. During food uptake, they were submitted to more than 10 full rotations. Self-generated positional information having been jammed, the animals no longer oriented towards the nest. By contrast, when the subjects were rotated at the food source and then briefly presented with the familiar visual environment, before the initiation of homing, they returned significantly towards the nest. However, their homing performance was less accurate than in control trials involving neither rotations nor the opportunity for a visual fix. Our results suggest that the visual fix provided the animals with directional, but not positional information.

HEER Lorenz

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Rank-specific mate expenditure of males in the polygynandrous Alpine Accentor (*Prunella collaris*)

By grouping and cooperating for territory defense, male Alpine Accentor of one breeding unit get into conflict for the access to fertile females within their group. Dominant males (alpha, sometimes beta) invest most in direct competition (social hierarchy, mate guarding, frequent copulations), while subordinate males are mostly restricted therefrom and invest more in the indirect competition (song, sitting self-advertisely). Dominant males are present full-time in their territory guarding a fertile female. Subordinate males spend only part-time in the territory and are preponderant present therein during the time of the 'insemination window'. Accordingly, dominant males sire most of the young.

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Phylogeny of Eucestoda: morphological and molecular congruence

Advances in our understanding of relationships among the 12 orders of the Eucestoda have been achieved based on independent approaches linked to comparative morphology and analysis of sequence data from 18s rDNA. Historically, the phylogeny for tapeworms has been problematic; numerous conflicting hypotheses have been presented over the past century. Recent studies indicate that resolution of relationships among the 12 orders appears near at hand. Maximum parsimony analysis of morphological and molecular databases yielded largely congruent trees supporting monophyly for the Eucestoda. Monozoic Caryophyllidea are the basal taxon; difossate forms such as the Pseudophyllidea are primitive; tetrafossate groups including the Tetraphyllidea, Proteocephalidea, Nippotaeniidea, Tetrabothriidea and Cyclophyllidea are highly derived. Hypotheses differed in the placement of the Trypanorhyncha and the Diphyllidea. These studies are a robust foundation for resolution of higher-level relationships among the tapeworms linked to 'total evidence' analyses. Through a top-down approach this has also supported phylogenetic studies among families of Cyclophyllidea, the most diverse and economically significant group of tapeworms in avian and mammalian hosts. Comparative data from morphology, ontogeny and ultrastructure are validated; a complementary nature for morphological and molecular approaches is emphasized. Phylogenetic data bases for the eucestodes represent model systems for evolutionary biology, cospeciation analysis and historical biogeography.

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Molecular, morphological and ecological evidence for species recognition in *Ammonia* (Foraminifera)

The genus *Ammonia* is one of the most common shallow water benthic foraminifers. Taxonomic identification of *Ammonia* species, however, is impeded by their great morphologic variability. In the present study, we combined molecular, morphological and ecological data to define two *Ammonia* species, termed *Ammonia* sp. 1 and *Ammonia* sp. 2. We obtained partial large subunit ribosomal DNA (LSU rDNA) sequences from 42 living specimens collected from the Mediterranean Sea, North Atlantic and South Pacific. DNA sequence analysis confirms that *Ammonia* sp. 1 and *Ammonia* sp. 2 form two genetically distinct species. Cluster analysis of their morphological characters shows that both species differ by the size of their tests and size of wall perforations. They may also be adapted to different environmental conditions as suggested by differences in their distribution in the Lagoon of Venice.

HOSKEN David

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Aspects of sperm competition in yellow dungflies

Sperm competition occurs when the ejaculates of different males compete to fertilize a given set of a females ova. How ejaculates compete is generally inferred from paternity data and mathematical modelling rather than by direct observation. Yellow dungflies are particularly well studied in this respect. Female dungflies store sperm in fixed volume sperm stores (spermathecae), and models of dungfly sperm competition suggest constant random sperm displacement with instantaneous mixing from the stores when females copulate more than once, with each subsequent male displacing about 80% of the previous stored sperm. However, histological evidence suggests some model assumptions are possibly incorrect, and examination of the large female accessory glands indicates functions not previously described. Furthermore, since males vary consistently in sperm length it is possible to use sperm length variation in the female sperm stores as a means of testing the current dungfly sperm competition model: if random displacement with instantaneous mixing occurs it is unlikely that the sperm from more than two males would be detected in the spermathecae. The variance in sperm length in samples from field captured females was compared to expectations based on variance distributions generated using sperm length data from field captured males. It appears females contain sperm from more males than expected with 80% displacement.

JOUSSON Olivier, BARTOLI Pierre & PAWLOWSKI Jan

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Use of the ITS rDNA for elucidation of the life cycles of Mesometridae (Trematoda, Digenea)

Identification of larval stages is crucial for elucidating the life cycles of various Digenea. However, in many digenean species, the larvae are morphologically indistinguishable and it is very difficult to establish the affiliation between the larval and adult stages by using the morphological criteria. The molecular methods, based on DNA sequencing or PCR-RFLP analysis, can offer a new tool for larval stage identification. In this study, the sequences of internal transcribed spacer of the ribosomal DNA (ITS rDNA) were used to identify the cercariae of three out of five species of the family Mesometridae (*Centroderma spinosissima*, *Elstia stossichianum*, and *Wardula capitellata*). These species differ among the others by the number of repeats in the ITS1 region. The phylogeny of Mesometridae was inferred from their ITS rDNA sequences.

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Eggs as a subject of phylogenetic research in Paussinae (Coleoptera: Carabidae)

The ant nest beetles (Paussinae) are a monophyletic taxon of approximately 450 myrmecophilous species. Together with Metriinae, Ozaeninae and Protopaussinae they form the monophyletic paussine complex within the ground beetles.

Despite the conspicuous structural diversity of the Paussinae, the external characters of the adults are insufficient to reconstruct well-founded genealogical relationships of the main lineages. The monophyly of the individual tribes and subtribes, however, is proven by several synapomorphic character states each. Preliminary studies indicate that the chorion structure of

the eggs may represent a good character for the phylogenetic reconstruction of the Paussinae. We distinguished two different types of chorion:

- A) Chorion thin, without aerenchym, netlike. A similar chorion type 'A' exists in several sub-families of the Carabidae representing lineages without close relationship (examined taxa: Brachininae (*Pheropsophus*), Carabinae (*Carabus*), Paussinae: Paussini (*Paussus*)). These findings indicate that this type of chorion structure represents an ancestral (plesiomorphic) character state within the Paussinae.
- B) Chorion thick, with spongiformous intrachorionic aerenchym. So far, this particular structure was only found in three tribes of Paussinae (examined taxa: Cerapterini (*Cerapterus*), Heteropaussini (*Heteropaussus*), Pentaplatarthrini (*Pentaplatarthrus*)). The currently available results indicate that this structure represents the first known shared-derived character state (synapomorphy) of these three taxa.

All figured eggs were recovered by dissection of dried or alcohol-preserved specimens.

LOCHER Rolf & BAUR Bruno

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Is the sperm pool in the hermaphroditic land snail *Arianta arbustorum* limited?

Many species of gastropods have different forms of sperm storage which provide the potential for sperm competition. However direct evidence for sperm competition is so far lacking, except in the simultaneously hermaphroditic land snail *Arianta arbustorum*. In this species multiple mating, multiple paternity and differential male fertilization success has been demonstrated. Sperm number is an important feature in sperm competition. We conducted a mating experiment to examine how long individuals of *A. arbustorum* need to recover from sperm depletion after a copulation. The results show that a delay of 8 and more days between two matings is enough to replenish the sperm reserves entirely. Furthermore, egg laying between two matings had no effect on the number of sperm transferred in the second copulation regardless the intermating interval. These findings contribute to a better understanding of sperm competition and sex allocation in simultaneous hermaphrodites.

LUGON-MOULIN Nicolas, GOUDET Jérôme, BRÜNNER Harald, WYTENBACH Andréas & HAUSSE Jacques

Institute of Zoology and Animal Ecology; Biology Building; University of Lausanne; CH-1015 Lausanne-Dorigny; Switzerland

Microsatellites reveal the fine-scale structure of a hybrid zone in *Sorex araneus* (Insectivora, Soricidae)

The common shrew (*Sorex araneus*) is subdivided into numerous chromosome races and several interracial hybrid zones have been discovered. Microsatellites were used to unravel the fine-scale genetic structure of a hybrid zone between chromosome races Valais and Cordon located in the French Alps. A total of 269 individuals collected between 1992 and 1995 were typed for seven microsatellite loci. Several approaches were used to study genetic structuring. We introduce the exact *G*-test to microsatellite data. The exact *G*-test was recently shown to be a powerful test of differentiation for diploid populations. Gene flow is clearly reduced between these chromosome races and has been estimated at one migrant every two generations using *R*-statistics and one migrant per generation using *F*-statistics. Hierarchical *F*- and *R*-statistics are compared and their efficiency to detect inter- and intraracial patterns of divergence is discussed. Within-race genetic structuring is significant, but remains weak. F_{ST} display similar values on both sides of the hybrid zone, although no environmental barriers are found on the Cordon side, whereas the Valais side is divided by several mountain rivers. A modified version of the classical Multiple Correspondence Analysis (CRT-MCA) is carried out. This analysis

clearly shows the dichotomy between the two races. Further analyses are realized to assess the genetic background of karyotypic hybrids to compare it with the genetic background of pure parental forms. Our results indicate that these karyotypic hybrids represent the trace of an ancient hybridization event.

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Genetic differentiation of the common toad (*Bufo bufo*) in the Alps

Bufo bufo occurs throughout Europe (except in northern Scandinavia) and in parts of northern Africa and western Asia. In the Swiss Alps, it is found up to 2200 m above sea level. Three subspecies are recognized. Two of them occur in our study area. *Bufo b. spinosus* is found in the Mediterranean region and *B. b. bufo* in the other parts of Europe, including the north of the Alps. We analyse the genetic differentiation of 30 populations of both subspecies in the Alpine region, using horizontal starch gel electrophoresis of ten enzymes from tadpoles. For comparison, we include three populations from more distant localities: Doupov (Bohemia, Czech Republic, *B. b. bufo*), Genova (Italy, *B. b. spinosus*), and Arles (Provence, France, *B. b. spinosus*), respectively.

A very low level of genetic differentiation is found among the populations from the Alpine region, including the *B. b. bufo* population from Bohemia and the *B. b. spinosus* populations from southern Switzerland and Genova. All these populations form a compact cluster in the dendrogram (UPGMA, using Nei's genetic distance in pairwise comparisons of populations as matrix for cluster construction). However, the Provence *B. b. spinosus* population is clearly differentiated from this cluster.

MIZRAHI-MEISSONNIER Liliana, FLOOK Paul K. & ROWELL C. H. F.

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Comparison of the utility of different data partitions of the 28S rRNA for the reconstruction of caeliferan phylogeny

We amplified and sequenced 2300 base pairs of the 28S ribosomal RNA gene in 50 caeliferan species (Insecta: Orthoptera). The sequenced region includes variable regions D1-D7b variable regions (based on the *D. melanogaster* model of Hancock, 1988), and 4 hypervariable regions. After calculating the secondary structure for the orthopteran 28S gene we partitioned the data according to pairing properties of different positions. We also partitioned data according to the pattern of sequence conservation and reconstructed phylogenies from different data sets. We then used objective criteria (e.g. consistency indices, nonparametric bootstrapping) to assess the utility of different regions of the 28S gene for phylogenetic reconstruction. Using the most informative character set we show that the 28S gene is useful for resolving phylogenetic relationships among the basal groups of the caeliferan Acridomorpha.

MONSUTTI Alice, PERRIN Nicolas, NACIRI-GRAVEN Yamama & GOUDET Jérôme

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Selection and life-history responses to size-dependent predation in *Physa acuta* (Gastropoda)

In order to investigate the evolutionary response of life-histories to a size-dependent predation, we performed two long-term (20 months) laboratory experiments involving the freshwater snail *Physa acuta*.

1. A selection experiment on juvenile length - simulating predation - resulted in a significant response in the line selected for larger size, as well as correlated responses for growth rate, size at maturity, and asymptotic size.
2. The second experiment involved controlled predation by two flatworm species on artificial populations, and also showed a significant increase in juvenile size in the populations under predation.
3. These two results show that important life-history parameters of the species under study may evolve quite rapidly (12 generations) under size-dependent predation.

MONTROYA-BURGOS Juan-Ignacio & PAWLOWSKI Jan

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Enlightening the history of Neotropical river systems by using loricariid catfish phylogeny

The catfish family Loricariidae (Siluroidei) includes more than 600 species inhabiting almost all Neotropical freshwater systems. The analysis of loricariids phylogeny is used here to unravel some aspects of paleohydrogeography in Tropical South America. We have sequenced the ITS1 - 5.8S - ITS2 region for several representatives of eight closely related loricariid genera. Three lineages have been identified in our phylogenetic tree. Within each lineage, the combination of present geographical distribution of species and their phylogenetic relationships is discussed. The results are compared to current knowledge on past drainage patterns.

MÜHLHÄUSER Claudia & BLANCKENHORN Wolf U.

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Female choice for larger males in the dung fly *Sepsis cynipsea* - Fisher's runaway or good genes?

In *Sepsis cynipsea* females show a characteristic vigorous shaking behaviour to dislodge the male on her back trying to copulate. We investigated the mechanisms of sexual selection in the laboratory. In a mate choice experiment we showed that females preferred larger males, and that copulations with larger males ensued faster.

Female choice was expressed in the duration of her shaking. The full sib heritability of head width (i.e. body size) was high, as expected. Female shaking duration was also heritable. The crucial genetic correlation between male size and female shaking (i.e. choice) was nil, however either due to low sample sizes, because it does not exist, or because of a genetic constraint suggested by the genetic correlation structure. We have evidence that large body size indicates good genes, as large males have a higher larval survival, large females enjoy a higher fecundity, and larger individuals of both sexes benefit from a longer adult life. The data support the good genes hypothesis as both preference and trait are heritable, and as there are fitness benefits other than mating success. Although the genetic correlation of trait and preference was not substantiated by our data, we cannot exclude that the Fisher process is also partly responsible for the evolution of this mating system.

MÜLLER Sonia

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Genetic diversity and relationships in the neotropical catfish genus *Ancistrus* (Siluriformes, Loricariidae) as revealed by allozyme electrophoresis

Genetic differentiation was examined among 46 samples of *Ancistrus* representing 15 putative species from the main cis-Andean river systems. Further samples of other Ancistrinae genera

were examined for outgroup comparison. Protein electrophoresis were performed on polyacrylamid gels using a Pharmacia Phastsystem; the gels were stained for 8 enzyme systems. All of the 11 presumptive loci analysed are polyallelic. Fixed allelic differences at 4 loci demonstrate the existence of two syntopic species which were not diagnosed by morphology. High variability is showed in populations of a largely sampled species from Amazonian and Paraguayan systems. The genetic distances are compared in regard to taxonomic distinctiveness. Hypothesis of phylogenetic relationships are given using phenetic and cladistic methods.

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The evolution of pollen heteromorphism in *Viola*: a phylogenetic approach

Pollen heteromorphism (the production within a plant of several pollen morphs that differ in aperture number) occurs in 30% of Angiosperm species. Variation in aperture number may be selected, because the aperture is the only point of the pollen wall where the pollen tube germinates. We have focused on the evolutionary significance of pollen heteromorphism in the genus *Viola* in which about 1/3 of the 500 recorded species are pollen heteromorphic. In several species of *Viola*, the different pollen morphs have different fitnesses: aperture number is positively correlated with germination speed, but negatively with life expectancy. We aim to study the distribution of pollen heteromorphism in *Viola* and to understand which selective pressures act on its maintenance, using a molecular phylogeny based on ITS sequence data. Taxonomic studies on *Viola* distinguish two main groups: Violets and Pansies, based on differences in flower morphology; Pansies are monophyletic, Violets are polyphyletic. Pollen heteromorphism has evolved independently at least 7 times in *Viola*. Variations in sporophytic ploidy level are linked to the apparition of pollen heteromorphism in all groups of Violets, not in Pansies. The proportion of pollen-heteromorphic species, variance in mean aperture number and range of variation of pollen morphs is significantly higher in Pansies than in all Violet groups. Together with predictions of the theory about the maintenance of pollen heteromorphism, this suggests that selective pressures may render pollen heteromorphism adaptive in Pansies, not in Violets. Our data indicate that its maintenance and development are probably contingent upon several prerequisites such as fitness differences between the different pollen morphs, pollination conditions and traits of flower morphology, which differ between Pansies and Violets.

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Mitochondrial DNA sequences as a means to deduce human history

DNA sequences from archaeological and palaeontological finds could potentially contribute substantially to our understanding of human history. However, most human remains are devoid of endogenous sequences that can be amplified by PCR. In those cases, contamination by contemporary human DNA poses serious problems. In the small proportion of remains where endogenous DNA exists, chemical degradation and modification make the retrieval of ancient DNA sequences difficult. For example, large amounts of oxidative base damage is present in most samples and correlate with the inability to amplify sequences. In order to overcome some of these problems, we have used HPLC to analyze the state of racemization of amino acids in ancient remains. This allows large numbers of samples to be screened in order to identify those where the state of conservation of amino acids suggests that DNA retrieval may be possible. By this approach, samples from the Neandertal type specimen were analyzed and a mitochondrial DNA sequence was determined by sequencing clones from short overlapping PCR products. Our experience with this and other ancient remains will be reviewed.

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Morphology and molecules in conflict: the phylogenetic relationship of *Callimico* within the Callitrichidae

The New World monkeys are divided into two main groups, Callitrichidae and Cebidae. Recent morphological phyletic studies generally place *Callimico* as the most basal offshoot within the Callitrichidae. By contrast, genetic studies have consistently placed *Callimico* somewhere within the Callitrichidae, not basal to this clade. In addition, the detailed nodal relationships of the two tamarin genera, *Saguinus* and *Leontopithecus*, remain controversial. A DNA sequence data set from a subfragment of the mitochondrial ND4 gene and the tRNA^{His}, tRNA^{Ser}, and tRNA^{Leu} genes was generated in an attempt to clarify the phylogenetic relationships within the Callitrichidae. We extracted DNA from hair or tissue samples from 8 species (*Ateles geoffroyi*, *Callimico goeldii*, *Callithrix jacchus*, *Cebuella pygmaea*, *Cebus apella*, *Leontopithecus rosalia*, *L. chrysomelas*, and *Saguinus midas*), amplified the fragment containing those genes by PCR and directly sequenced the template. Additional data from outgroup taxa were available from GenBank. The 887 bp sequences were analysed by maximum parsimony, neighbor-joining, and maximum likelihood methods. The main results are that the phylogenetic position of *Callimico* is resolved between the marmosets (*Callithrix*, *Cebuella*) and the tamarins (*Saguinus*, *Leontopithecus*), while *Leontopithecus* and *Saguinus* together form the most basal clade of the Callitrichidae. Combined analyses of all previously published nuclear and mitochondrial gene sequences (5201 base pairs) confirm these results. As available molecular evidence indicates that *Callimico* is more closely related to the marmosets than to the tamarins, a reconsideration of the morphological evidence in the light of the consensus tree from DNA sequence analyses is warranted.

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Calibrating ribosomal clocks in foraminifera

Because of their well known fossil record, foraminifera offer unusual opportunity to provide temporal dimension to the molecular phylogeny and to study the tempo and mode of molecular evolution. In order to test the current palaeontological hypotheses on evolution of foraminifera, we have obtained partial SSU rDNA sequences of 50 benthic and 18 planktonic species. By comparing the number of substitutions with the divergence times inferred from the fossil record we evaluated absolute rates of rDNA evolution for several species. Our study reveals important differences in rates of molecular evolution between different groups of foraminifera, ranging from 4.0×10^{-9} subst./site/year in planktonic species to less than 0.1×10^{-9} subst./site/year in some benthic species. However, with few exceptions, the rates are relatively stable within two planktonic (Globigerinidae, Globorotaliidae) and one benthic (Soritidae) families, suggesting that the local ribosomal clocks may exist in foraminifera.

PERRET Mathieu, SOVALAINEN Vincent, CHAUTES Alain & SPICIGER Rodolphe

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Evolution of pollination systems in Sinningieae (neotropical Gesneriaceae); insights from molecular phylogenetics

The study of long-term patterns and processes of organisms diversification is a major challenge in evolutionary biology and ecology. In this context, we intend to study the evolution of plant-

pollinator systems within Sinningieae (Gesneriaceae). This tribe, distributed throughout the Neotropics, includes herbaceous plant and shrubs which are pollinated by a wide range of animals like bees, butterflies, moths, hummingbirds and bats. The systematic, morphological diversity and geographical distribution of the Sinningieae are well studied, but little has been done to understand how ecological relationships with their pollinators originate and evolve. To study these mechanisms, we intend to map the pollination systems onto an accurate phylogeny and to trace the evolutionary events that have given rise to the modern distribution of ecological features. Until now, half of the currently described species have been collected for which the trnL-trnF and rbcL-atpB chloroplast intergenic spacer has been sequenced. Our intention is to present probable evolutionary scenarios (multiple syndromes) that can be inferred from the molecular phylogeny, and discuss them in the light of the actual morphological and biogeographical knowledge.

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Evaluation of dry grassland management using spider communities

In Switzerland, the inventory of dry grasslands, with the aim to protect these semi-natural habitats, has triggered interest in studying the effects of their management on their fauna. A special emphasis is put on spiders, since they are one of the most important groups of terrestrial predators, and, thanks to their diversity and abundance, they are known as good bioindicators of the ecological state of their habitat.

In 1995 and 1996, we worked on 40 sites on the Swiss occidental plateau, collecting spiders by means of pitfall traps. The evaluation method used takes into account biotop fidelity and the rarity of the species. This method privileges the specificity of the population in relation to its present habitat. Therefore, it allows us to not underestimate the quality of the biotops, which although very homogeneous, comprise very few species but for whom the ties with their surroundings are very close (stenoeccious species) and at the same time not to over-estimate the stations rich with ubiquitous (euryoeccious) species.

This study allows us to discuss the different management strategies. For dry grasslands conservation, it seems important to upkeep them extensively. This operation must be done late in the year (autumn). In addition, we recommend to divide the surface of a dry grassland in order to alternate the upkeep. This way of management allows us to maintain an abandoned part indispensable for some species to carry out their life cycle. The continued study of certain stations showed the capacity of spiders to reflect the effects of management. In future, it seems important to use spiders for research in habitat descriptions and evolutions together with phytosociological transects.

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Genetic, environmental and condition-dependent effects on female and male ornamentation in the barn owl *Tito alba*

In birds, usually the males only are ornamented. Interestingly, in the barn owl *Tito alba* both female and males display sex-limited plumage traits. Males are commonly lighter coloured, and females spottier. A partial cross-fostering experiment tested the relative importance of shared genes and a shared environment for the resemblance of related birds. Siblings raised in different nests converged towards similar trait values, offspring resembled the true but not the foster parents, and plumage traits of unrelated nestlings sharing the same nest were not correlated. Results were not inflated by maternal effects detectable in the mother's phenotype, since mid-daughter to mother resemblance was not higher than mid-son to father resemblance. This suggests the plumage coloration and spottiness are largely genetically inherited traits, and that

the rearing environment has not a strong impact on the expression of these traits. The further investigate whether the two sex-limited traits are condition-dependent, brood sizes were manipulated. Enlargement or reduction of broods by two nestlings resulted in lower and higher body mass of nestlings respectively. However, nestlings raised in enlarged or reduced broods did not show a significantly darker or lighter, or a more or less spotted plumage. No genotype by environment interaction was detected. In conclusion, additive genetic variance for plumage coloration and spottiness is maintained, and both the rearing environment and brood condition do not account for a large proportion of the phenotypic variance in female and male ornamentations.

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Identifying ambiguous landmarks through vector addition

Path integration (PI) is the process by which an animal uses information about its own movements in order to keep track of its current position relative to the starting point of its trip. PI and stable spatial information (such as memorized landmarks) complement each other. In particular, PI can help the animal solve the problem of locating a goal specified by ambiguous landmarks. An experiment was devised to test this.

Each subject (hamsters) inhabited a round, optically shielded arena with a peripheral nest. There were four identical cylinders in a square pattern around the arena centre. One of the cylinders (always in the same position relative to the nest) was baited with food, and the animal was trained to climb into it and hoard the food. This allowed the animal to establish a long-term memory of the location of the baited cylinder relative to the nest. In test trials, the animals were lured in darkness along the periphery of the arena, then the lights were switched on, and the animal could now see the array of cylinders under a new perspective. Only by keeping track of its own movements could the animal identify which, among the four visually indistinguishable cylinders, was the correct one. Results indicate that the animal can indeed combine PI to a memory of goal position in order to reach the goal from novel points. This is akin to saying that the animal can vectorially add its current position vector to the vector stored in long-term memory.

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Molecular phylogeography: A glimpse to the past of a Pocket Gopher hybrid zone

Mitochondrial DNA (mtDNA) variation in the cytochrome b gene was determined for two divergent taxa of pocket gophers, *Thomomys bottae actuosus* and *T. b. ruidosae*. These two taxa hybridize in a narrow contact zone in New Mexico (USA), but introgression of nuclear markers such as allozymes or chromosomes does not extend much beyond the hybrid zone. We found that despite their distinctness, the two subspecies shared very similar mtDNA haplotype. By a comparison of phylogenetic histories derived from nuclear markers (allozymes) and from mtDNA haplotypes sampled in different populations of *T. bottae* from New Mexico, we show that apparent similarity is due to an introgression of *T. b. ruidosae* mtDNA into *T. b. actuosus* nuclear background. Evidence of introgression is not limited to the present-day contact zone between these two taxa, but extends at least 75 km away from it. Of several potential mechanisms which could lead to such a geographic pattern of variation, we argue that a combination of range shifts due to climatic fluctuations, and genetic drift are most likely. We also discuss why selection, which might have promoted the spread of one haplotype across the hybrid zone, is a less likely explanation. Horizontal gene transfers due to hybridization are not uncommon historical events among animals and plants. Although they can be identified with careful phylogenetic study using independent data sets, the potential for misinterpreting a gene tree as an organismal tree is great.

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Phylogenetics of flowering plants based upon a combined analysis of plastid *atpB* and *rbcL* gene sequences

In plant molecular systematics, since the broad scale *rbcL* analysis of Chase, Soltis, Olmstead *et al.*, there has been much debates on the use of such large datasets. Recently, Hillis showed using simulations based on a new 18S dataset from Soltis *et al.*, that recovering complex phylogenies were surprisingly easier than previously thought. We present here a new phylogenetic analyses for angiosperms, based upon the *atpB* and *rbcL* chloroplast gene sequences for 358 taxa representing all major lineages. The results obtained by combining these genes, the feasibility of such analyses as well as the support/resolution of these phylogenies are presented.

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Population dynamics of lynx in relation to its prey - A comparison between Canada and Europe

Periodic fluctuations of mammalian populations and their potential causes have received considerable attention. One of the main hypothesis concerning predator-prey dynamics predicts that only populations of specialist predators follow the population fluctuations of their prey. The lynx (*Lynx lynx*) populations in Canada and Europe are an ideal system to test this hypothesis. The Canadian lynx is a specialist predator and its main prey, the snowshoe hare (*L. americanus*), shows periodic population fluctuations. The European lynx is a generalist with a diverse diet including roe deer (*C. capreolus*), reindeer (*Rangifer tarandus*) and red deer (*Cervus elaphus*). Therefore the European lynx should not show any periodic or even cyclic population fluctuations relative to its prey. I tested this hypothesis by analysing the hunting statistics of lynx shot in Norway from 1846-1980 and population size estimates from the lynx in Białowieża Primeval Forest in Poland (1958-1994) with time series analysis. No regular or even cyclic fluctuations of the European lynx populations could be detected, in either population. These results support the hypothesis that only populations of specialist predators follow the population fluctuations of their prey.

SCHNEIDER Stefan & EXCOFFIER Laurent

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Estimation of past demographic parameters using the mismatch distribution

The distribution of pairwise differences between the sequences observed in a sample (the mismatch distribution) can be very informative about the recent demographic history of the population (Rogers and Harpending, 1992). The theoretical model developed by Li (1977) describing the expected mismatch distribution was based on the infinite sites model and assumed the homogeneity of mutation rates over the sequence. However in the control region

of human mitochondrial DNA, quite large amount of heterogeneity of mutation rates has been observed (Wakeley 1993). In this case, because most mutations occur at a small number of loci, the effect of reverse mutations cannot be neglected. To take into account this effect, we have extended a model introduced by Yang (1996), to provide the expected mismatch distribution under more realistic conditions. We thus explicitly take into account the finiteness of the sequence under consideration, the transition bias observed for mtDNA, and up to 4 different mutation rates in the sequence. We also provide a way to compute confidence intervals for the estimated parameters (population size before and after the expansion and the time elapsed since the expansion), as well as for the expected mismatch distribution. We apply this new methodology to the case of human mtDNA.

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SCHNEITER Beat & SAUCY Francis

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Juvenile dispersal in the vole *Arvicola terrestris* (Rodentia, Arvicolidae) during rainy nights

Abnormally high densities recorded in enclosed populations of small mammals suggest that dispersal may be an important component of their population dynamics. For practical reasons, dispersal is a difficult phenomenon to address because it is uneasy to distinguish dispersers from residents.

Previous studies conducted using the classical below-ground trapping approach have shown that fossorial *Arvicola terrestris* move mostly over short distances, but high turnover of young individuals suggest that our understanding is still incomplete. Taking advantage of the fact that this vole usually lives in underground tunnels, we have attempted to catch individuals dispersing above the ground in traps set along drift fences. Observations were conducted in two permanent grasslands where we fenced two 50 x 50 m trapping grids. Fences were also established along the edges of neighbouring forests. Two unfenced grids served as controls. From March to July 1997, the average density of the below-ground populations increased approximately from 70 to about 250 ind/ha. A total of 734 captures and recaptures of 450 *A. terrestris* were recorded along the fences during 121 days of continuous trapping (March 22-July 20 1997). Interestingly, 91% of the voles caught above the ground were either juveniles or subadults, as compared to only 44% in our below-ground samples. No bias in sex-ratio could be found among dispersers. More surprisingly, most captures occurred during few rainy nights indicating that fossorial *A. terrestris* disperse *en masse* above ground during rainy periods.

SCHUCHERT Peter

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Phylogeny and Classification of the Hydrozoa (Cnidaria)

Traditional hydrozoan systematics is characterized by a primary dichotomy separating the Siphonophora from all other members of the class. The lack of complex characters, the frequent homoplasy, and their enormous morphological and life-history variation make the hydrozoans not an easy taxon for a phylogenetic analysis. Some progress towards a more natural classification has been made in recent years by recognizing that the Hydrocorallina (hydrozoans with a calcareous skeleton) are polyphyletic. In the present work, a phylogenetic analysis and classification is attempted. Even the few characters available evidently show that the traditional dichotomy Siphonophora versus Hydroidomedusae is no longer acceptable. While some of the

traditional orders like the Narcomedusae, Trachymedusae and the Thecata are recognized as monophyletic groups, the order Limnomedusae must be revised and the order Athecata-Anthomedusae must be abolished. The Siphonophora clearly belong to a clade named Gastrogonae containing also the former members of the Athecata as well as the Hydrocorallina. The following classification is proposed:

HYDROZOA: NARCOMEDUSAE
 MANUBRIOGASTRAE (new name)
 TRACHYMEDUSAE
 HYDROIDEA
 LIMNOMEDUSAE
 STOLONATA (new name)
 THECATA
 GASTROGONAE (new name).

SPICHTER Rodolphe & SAVOLAINEN Vincent

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Teaching botany in a molecular world

The application of molecular biology in botany has drastically changed our knowledge in systematics and evolution. The most recent systems of classification proposed by Takhtajan, Dahlgren, Thorne and Cronquist are questioned by molecular phylogenetics whereas these results are not yet fully accepted. However, molecular botany is now close to draw the picture of plant phylogeny since large datasets are currently analysed in several institutes. It is consequently a difficult period for the teaching of academic botany where modern results have to be integrated into the conventional classification. This poster is not a new classification of flowering plants since such work will be published later by the angiosperm phylogeny group. However we present a general picture of the angiosperms as based on our formal botanical course (using idiosyncratic terminology), according to affinities (mainly based on Chase *et al.*) and macroscopic features, and in comparison with the classifications of Cronquist and Thorne.

SWALLA Billie J.

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Evolution and Development of the Chordate Body Plan

Metazoan phyla are classified as either protostomes or deuterostomes based on morphological, phylogenetic and developmental studies. Deuterostomes have radial cleavage patterns, development of the embryonic blastopore into the adult anus and coelomic formation by enterocoely. Within the deuterostomes, chordates have a distinct body plan which is thought to have evolved from an ancestral deuterostome similar to extant hemichordates or urochordates, but studies of chordate evolution within the deuterostome phyla are hampered by the poor fossil record left by the soft-bodied ancestors. The urochordate ascidians possess definite chordate characteristics as tadpole larvae including a tail containing a dorsal neural tube, notochord, and muscle cells flanking the notochord. The head contains the sensory organs, a brain and most of the endoderm, or gut. We have used two closely related ascidian species with dramatically different larval phenotypes to look for genes involved in the specification of the chordate body plan during development. One of these genes, *manx*, appears to be a transcription factor that is necessary very early in development for the specification of tissues in the larval tail.

We have isolated several other maternal genes implicated in specifying the larval body plan, including *p58* and *cymric*. *P58* appears to be urochordate specific and is also implicated in autonomous muscle development. Recent studies conducted in my laboratory are aimed towards establishing a robust phylogeny of the deuterostomes, with special emphasis on the urochordates

and hemichordates. We will use this phylogeny to infer which organisms may closely resemble the ancestral chordates in an effort to understand the evolution of chordates. We will study the expression of genes we believe are involved in specifying the chordate body plan in extant embryos and larvae in an effort to understand which developmentally regulated genes may have been co-opted in a non-chordate ancestor to elaborate the chordate phenotype. Current progress on these studies will be discussed in my lecture.

TOURASSE Nicolas & GOUY Manolo

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Accounting for evolutionary rate variation among sequence sites consistently changes universal phylogenies deduced from rRNA and protein-coding genes

Identification of the primary lineages of life and of their evolutionary relationships is essential for understanding early cellular evolution, particularly the transition between prokaryotes and eukaryotes. Most molecular phylogenetic analyses of small subunit (SSU) and large subunit (LSU) ribosomal RNA sequences as well as analyses of isoleucyl-tRNA synthetase and of the largest subunit of RNA polymerase support the existence of three monophyletic domains, Archaea, Bacteria, and Eukarya. In contrast, analyses of elongation factors 1alpha/Tu and 2/G and of the second largest subunit of RNA polymerase suggested that Archaea are paraphyletic and that Eukaryota are specifically related to a subset of Archaea. Crenarchaeota (previously eocytes) as advocated by Lake. We have re-analyzed this question using the large numbers of sequences now publicly available and recently developed methods of phylogenetic analysis. These methods differ mainly from previous ones in using more realistic models of molecular evolution which account for the extensive variation among sequence sites of the rate of substitution. We report here that this approach gives considerable support to the crenarchaeote - eukaryote relationship, both from rRNA and protein sequence data.

VIZOSO Dita & LOSADA Freddy

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Effect of the habitat complexity on the size distribution of marine invertebrates

The spatial arrangement of the habitat, also known as spatial structure, may affect the body size distribution of the inhabitant organisms by constraining the available space. In spite of the generalized idea of the existence of such a relationship, methodological problems in the measurement of habitat complexity have constrained studies in this topic. In the present study, the size distribution of diverse and discrete communities of marine invertebrates was analyzed and correlated with the spatial complexity of the habitat. This complexity was represented by the fractal dimension of the sessile macroalgae that serve as habitat to the communities. The fractal dimension offers a direct measure of the ruggedness of a surface, thus allowing the quantitative characterization of the habitat complexity. The fractal dimension is scale-invariant. This feature allows the characterization of the habitat a different scales without bias in the measure, covering all the range of organisms that may be affected and offering a "organismal" point of view. The size of the invertebrates present different distributions according to the fractal dimensions of the studied macroalgae.

WÄCKERS Felix

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Extrafloral nectar production as a herbivore-induced plant defense

The effect of herbivory on the quantity of extrafloral nectar production, as well as its composition and distribution was studied in castor, cotton, and faba bean plants. In ricinus and cotton,

herbivore damage increased the total volume of secreted nectar by a factor 3 and 12 respectively. No significant increase due to herbivory could be measured in faba beans. Induction of nectar production was mainly restricted to the damaged leaf. Systemic effects were found in adjacent younger leaves only. The increased nectar production could be detected within 16 hours following the onset of herbivore feeding. The induced increase in nectar production ceased within 48 hours following herbivore removal.

WÜEST Jean

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The evolution of the pheromone dispersing apparatus in some Hesperidae (Lepidoptera)

Within the family Hesperidae, we studied the organization of the male pheromone dispersing apparatus, which is localized on the forewings, in 3 species, *Thymelicus lineola*, *Th. actaeon* and *Hesperia comma*. The organization of the apparatus, as well as the morphology of the androconias, present a growing degree of complexification, perhaps representing the way in which the apparatus and androconias were elaborated during evolution of this group. The apparatus is formed simply by patches of androconias in *Th. lineola*. In *Th. actaeon*, around the patches of androconias, the adjacent scales are slightly modified and orientated towards the androconial line. In *H. comma*, the patches of androconias are completely covered by the adjacent scales, which form a closed space above the androconias. In Hesperidae, the androconias are tubular scales containing the pheromone within the hollow medulla. These scales can break into pieces named osmophores, which are the dispersing mean of the pheromone. In *Th. lineola*, the scales are tubular and non-breakable, but some rare scales present constrictions which can be hypothesized as precursors of the dehiscent zones present in the two other species. In *Th. actaeon*, all the androconias present dehiscent zones and break into osmophores, but they often remain unbroken. In *H. comma*, all the androconias are broken and the liberated osmophores are glued together into a net just under the roof made of the adjacent scales.

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Parasites as selective agents in two host sister taxa: Prevalences of trematode infection in molluscan intermediate hosts in dependence of habitat factors

Adaptation to parasitism can be an important selective factor which determines distribution and relative abundances of closely related species. In this study the trematode communities infecting two closely related freshwater snails which differ in habitat choice and distribution, *Lymnaea peregra* and *L. ovata*, were examined in a field survey.

Trematodes commonly lead to complete castration of their molluscan intermediate host, thus the selective pressure imposed by these parasites upon snail populations is strong. The parasite life cycle involves further hosts, therefore factors external to snail populations are important to its maintenance.

Several habitat factors were tested for an impact upon parasite prevalences. The surrounding of a freshwater habitat, which might determine presence of end hosts, the substrate, which influences habitat choice of the snails, and habitat permanence showed the largest effects. Habitats with high prevalences were disproportionately often inhabited by *L. peregra*, the host with significantly more infections in total. The prevailing cercarial types were not the same in both snail species, suggesting that the snails differ in susceptibility to the various parasite types. *L. ovata* was far more abundant in the lowlands, while *L. peregra* was more abundant at higher altitudes. Sympatric sites were rare, and intermediate snail forms which would suggest hybridization were found extremely rarely.

Since parasite prevalences vary across habitat types, the snail species meet differential selection pressures for parasite resistance in the varying habitats, and separation through habitat specialization may be enhanced by parasites.

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Phylogeography of the vole *Arvicola terrestris* as revealed by mtDNA: The role of historical factors?

Arvicola terrestris is a large vole (family Arvicolidae) with a wide geographic distribution covering most Eurasia. It is a highly polymorphic species with more than 35 subspecies which can be grouped, according to their ecology, into aquatic and fossorial forms. Aquatic animals are large and live in wet lowlands, whereas fossorial ones are smaller and live in mountainous areas. Aquatic populations, transitionally colonising drier habitat, have often been described. Aquatic transitional populations show fossorial behaviour and adopt fossorial life-history traits. The origin of these forms which are differentiated by characters such as habitat, body size, colour, weight, population dynamics, home range size and mating behaviour is still controversial. In order to solve this problem, we studied allozyme and mitochondrial DNA polymorphism for aquatic and fossorial animals originating from populations from most parts of the geographic distribution of the species. Whereas morphology and habitat suggest some hybridisation between forms, the mitochondrial phylogeny, based on 150 sequences of 800bp of the cytochrome b gene, distinguish three main groups. Fossorial populations living in mountainous areas of Europe are monophyletic. Aquatic populations from the south of the Alps form a separate monophyletic clade which has probably emerged first from the aquatic ancestral pool of populations. Finally, the remaining populations of northern Europe, England and the east of Eurasia belong to the last most diversified clade. The fossorial clade seems to result from a single, more recent, historical differentiation coupled with some morphological and behavioural adaptive traits. Phylogeographic hypotheses will be discussed with the aim to propose a scenario which could explain the actual distribution of populations of *Arvicola terrestris* in relation to climatic events of the early Pleistocene.

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Molecular phylogenetic analysis of the tapeworm order Proteocephalidea based on mitochondrial 16S rDNA sequences

Systematics of the tapeworm order Proteocephalidea (Eucestoda) whose members are obligatory parasites of the alimentary tract of fishes, amphibians and reptiles has until recently been addresses using morphological and life-cycle data. These approaches failed so far to yield satisfactory results: other sources of characters, DNA sequences in particular, are being explored to better understand the evolution of this tapeworm order.

I attempt here to infer phylogenetic relationships among a variety of proteocephalidean representatives using a fragment of the mitochondrial 16S rDNA molecule. A 478 bp sequence was obtained for 41 proteocephalidean cestodes as well as for two outgroup species (a tetraphyllid and a cyclophyllid). 415 sites were unambiguously aligned, 115 of which were phylogenetically informative. Both parsimony and distance method-analyses yielded similar results:

- the two traditional families: Monticelliidae and Proteocephalidae are not recognised
- the monophyly of the type genus *Proteocephalus* is not supported, although a clade consisting of palearctic *Proteocephalus* species only is well defined, thus excluding species from the New World. Morphological features that distinguish the two groups of *Proteocephalus* need yet to be clarified
- resolution of relationships among the remaining Proteocephalidea is poor. Paucity of synapomorphies and high homoplasy indices ($HI=0.702$) leading to a large number of equally parsimonious trees account for this result.